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## SEQUENCE LISTING

<110> Schmitz, Oliver  
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 Wendel, Birgit  
 Kamlage, Beate  
 Plesch, Gunnar

<120> Method for Producing Amino Acids

<130> 13195-00006-US

<150> PCT/EP2003/014649

<151> 2003-12-19

<150> DE 102 61 188.2

<151> 2002-12-20

<160> 26

<170> PatentIn version 3.3

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Gly Arg Asp Pro Ser Cys Phe Arg Leu Glu Thr Glu Met Ala Lys Ile  
50 55 60

Leu Gly Lys Glu Gly Ala Leu Phe Val Pro Ser Gly Thr Met Ala Asn  
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Asn Lys Ala Lys Leu Leu Ala Asp Gly Leu Asn Glu Ile Lys Gly Leu  
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Arg Val Asp Ile Ser Ser Val Glu Thr Asn Ile Ile Tyr Val Glu Val  
50 55 60

Glu Glu Gly Ser Arg Ala Thr Ala Ala Lys Leu Cys Lys Asp Leu Glu  
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Asp Tyr Gly Ile Leu Leu Met Pro Met Gly Ser Ser Arg Leu Arg Ile  
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Lys Lys His Gly Leu Lys Leu His Ile Asp Gly Ala Arg Ile Phe Asn  
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65 70 75 80

Asp Ser Val Ser Val Cys Leu Ser Lys Gly Ile Gly Ala Pro Val Gly  
85 90 95

Ser Val Ile Val Gly Ser Lys Asn Phe Ile Ala Lys Ala Arg Arg Leu  
100 105 110

Arg Lys Thr Leu Gly Gly Gly Met Arg Gln Ile Gly Leu Leu Cys Ala  
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Gly Gly Gly Met Arg Gln Val Gly Ile Leu Cys Ala Ala Ala Tyr Val  
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Ala Val Arg Asp Thr Val Gly Lys Leu Ala Asp Asp His Arg Arg Ala  
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Lys Val Leu Ala Asp Gly Leu Lys Lys Ile Lys His Phe Arg Val Asp  
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Val Ile Leu Gly Asp Asp Ser His Ile His Ile Tyr Glu Asn Gly Gly  
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Glu Glu Met Ala Lys Met Met Gly Lys Glu Ala Ala Leu Phe Val Pro  
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Ser Gly Thr Met Gly Asn Leu Ile Cys Val Met Val His Cys Asp Val  
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aat atc gat ggg ttc tat gac aaa tta ttg gag ttc ctc aaa cac tct Asn Ile Asp Gly Phe Tyr Asp Lys Leu Leu Glu Phe Leu Lys His Ser 180 185 190			576
att caa gaa cgg ttc atc agt gtg aag aat ggt gaa atc att caa gtt Ile Gln Glu Arg Phe Ile Ser Val Lys Asn Gly Glu Ile Ile Gln Val 195 200 205			624
gcc tcc act ccg cag gaa gtt gtt gat aaa ata gag aag tac gtc gtt Ala Ser Thr Pro Gln Glu Val Val Asp Lys Ile Glu Lys Tyr Val Val 210 215 220			672
cca gag ggc cgt ttc aat ttg aat tgg agc gac gaa ggt cac gct cac Pro Glu Gly Arg Phe Asn Leu Asn Trp Ser Asp Glu Gly His Ala His 225 230 235 240			720
gag gat tgt gct aaa taa Glu Asp Cys Ala Lys			738

245

<210> 12  
 <211> 245  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 12  
 Met Thr Met Glu Lys Asn Gly Gly Asn Ser Ser Arg Gly Gly Gln Val  
 1 5 10 15  
 Gly Gly Lys Ser Val Cys Val Tyr Cys Gly Ser Ser Phe Gly Ala Lys  
 20 25 30  
 Ala Leu Tyr Ser Glu Ser Ala Glu Glu Leu Gly Ala Leu Phe His Lys  
 35 40 45  
 Leu Gly Trp Lys Leu Val Tyr Gly Gly Gly Thr Thr Gly Leu Met Gly  
 50 55 60  
 Lys Ile Ala Arg Ser Thr Met Gly Pro Asp Leu Ser Gly Gln Val His  
 65 70 75 80  
 Gly Ile Ile Pro Asn Ala Leu Val Ser Lys Glu Arg Thr Asp Glu Asp  
 85 90 95  
 Lys Glu Asp Val Asn Lys Ala Leu Leu Glu Ser Val Glu Asn His Lys  
 100 105 110  
 Gly Ala Thr Pro Ile Ser Glu Glu Tyr Gly Glu Thr Thr Ile Val Pro  
 115 120 125  
 Asp Met His Thr Arg Lys Arg Met Met Ala Asn Leu Ser Asp Ala Phe  
 130 135 140  
 Val Ala Met Pro Gly Gly Tyr Gly Thr Phe Glu Glu Ile Met Glu Cys  
 145 150 155 160  
 Ile Thr Trp Ser Gln Leu Gly Ile His Asn Lys Pro Ile Ile Leu Phe  
 165 170 175  
 Asn Ile Asp Gly Phe Tyr Asp Lys Leu Leu Glu Phe Leu Lys His Ser  
 180 185 190  
 Ile Gln Glu Arg Phe Ile Ser Val Lys Asn Gly Glu Ile Ile Gln Val  
 195 200 205  
 Ala Ser Thr Pro Gln Glu Val Val Asp Lys Ile Glu Lys Tyr Val Val  
 210 215 220  
 Pro Glu Gly Arg Phe Asn Leu Asn Trp Ser Asp Glu Gly His Ala His  
 225 230 235 240  
 Glu Asp Cys Ala Lys  
 245

<210> 13  
 <211> 1083  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> CDS  
 <222> (1)..(1083)  
 <223> Threonine aldolase

<400> 13  
 atg gta act aga att gtg gat ctt cgg tca gac aca gtt aca aag cca 48  
 Met Val Thr Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro  
 1 5 10 15  
 act gaa gca atg aga gct gct atg gca agt gct gaa gtt gat gac gat 96  
 Thr Glu Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp  
 20 25 30  
 gtt cta ggc tat gat cca act gct ttt cgc tta gaa aca gag atg gca 144  
 Val Leu Gly Tyr Asp Pro Thr Ala Phe Arg Leu Glu Thr Glu Met Ala  
 35 40 45  
 aag aca atg ggc aaa gaa gct gct ctt ttt gtt cca tct ggc act atg 192  
 Lys Thr Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met  
 50 55 60  
 ggg aac ctt gta tct gta ctt gtt cat tgt gat gtc agg gga agt gag 240  
 Gly Asn Leu Val Ser Val Leu Val His Cys Asp Val Arg Gly Ser Glu  
 65 70 75 80  
 gtt att ctt gga gac aat tgc cat atc aac att ttt gag aat gga ggc 288  
 Val Ile Leu Gly Asp Asn Cys His Ile Asn Ile Phe Glu Asn Gly Gly  
 85 90 95  
 att gca acc att ggg gga gtg cat cca aga caa gtg aaa aat aac gat 336  
 Ile Ala Thr Ile Gly Gly Val His Pro Arg Gln Val Lys Asn Asn Asp  
 100 105 110  
 gat gga acc atg gac att gat ttg att gag gct gct atc agg gac cca 384  
 Asp Gly Thr Met Asp Ile Asp Leu Ile Glu Ala Ala Ile Arg Asp Pro  
 115 120 125  
 atg ggg gag cta ttc tat cca acc acc aag ctt att tgc ttg gaa aat 432  
 Met Gly Glu Leu Phe Tyr Pro Thr Thr Lys Leu Ile Cys Leu Glu Asn  
 130 135 140  
 act cat gca aac tct ggt ggc aga tgc ctc tca gtt gaa tat aca gac 480  
 Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Val Glu Tyr Thr Asp  
 145 150 155 160  
 aga gtt gga gag tta gct aag aag cat gga ctg aag ctt cac att gat 528  
 Arg Val Gly Glu Leu Ala Lys Lys His Gly Leu Lys Leu His Ile Asp  
 165 170 175  
 ggg gcc cgt att ttt aac gca tca gtt gca ctt ggt gtt cca gtg gat 576

Gly	Ala	Arg	Ile	Phe	Asn	Ala	Ser	Val	Ala	Leu	Gly	Val	Pro	Val	Asp		
			180					185					190				
agg	ctt	gtc	cag	gcg	gct	gat	tca	gtt	tcc	gtt	tgc	cta	tct	aaa	ggc		624
Arg	Leu	Val	Gln	Ala	Ala	Asp	Ser	Val	Ser	Val	Cys	Leu	Ser	Lys	Gly		
		195					200					205					
ata	ggc	gct	cca	gtt	gga	tct	gtt	att	gtt	ggc	tcc	aag	aat	ttt	att		672
Ile	Gly	Ala	Pro	Val	Gly	Ser	Val	Ile	Val	Gly	Ser	Lys	Asn	Phe	Ile		
	210					215					220						
gcc	aag	gct	aga	cga	ctc	cgg	aaa	acc	tta	gga	ggc	gga	atg	aga	cag		720
Ala	Lys	Ala	Arg	Arg	Leu	Arg	Lys	Thr	Leu	Gly	Gly	Gly	Met	Arg	Gln		
225					230					235					240		
att	ggc	ctc	ctt	tgt	gcc	gct	gca	ctt	gtt	gcc	ttg	cag	gaa	aat	gtt		768
Ile	Gly	Leu	Leu	Cys	Ala	Ala	Ala	Leu	Val	Ala	Leu	Gln	Glu	Asn	Val		
				245					250					255			
ggg	aag	ctg	gaa	agt	gat	cac	aag	aaa	gct	aga	ctt	ttg	gct	gat	gga		816
Gly	Lys	Leu	Glu	Ser	Asp	His	Lys	Lys	Ala	Arg	Leu	Leu	Ala	Asp	Gly		
		260					265						270				
tta	aac	gaa	gtt	aaa	gga	ttg	aga	gtg	gat	gcc	tgt	tct	gtg	gag	acc		864
Leu	Asn	Glu	Val	Lys	Gly	Leu	Arg	Val	Asp	Ala	Cys	Ser	Val	Glu	Thr		
		275					280					285					
aat	atg	gta	ttt	att	gac	att	gaa	gag	ggc	aca	aag	act	aga	gca	gaa		912
Asn	Met	Val	Phe	Ile	Asp	Ile	Glu	Glu	Gly	Thr	Lys	Thr	Arg	Ala	Glu		
	290					295					300						
aag	ata	tgc	aag	tac	atg	gaa	gaa	cgt	ggc	atc	ctt	gtg	atg	caa	gag		960
Lys	Ile	Cys	Lys	Tyr	Met	Glu	Glu	Arg	Gly	Ile	Leu	Val	Met	Gln	Glu		
305					310					315					320		
agt	tca	tca	aga	atg	aga	gtt	gtt	ctc	cat	cac	caa	ata	tca	gca	agt		1008
Ser	Ser	Ser	Arg	Met	Arg	Val	Val	Leu	His	His	Gln	Ile	Ser	Ala	Ser		
				325					330					335			
gat	gtg	caa	tat	gcc	ttg	tcg	tgc	ttt	cag	caa	gct	cta	gct	gtc	aaa		1056
Asp	Val	Gln	Tyr	Ala	Leu	Ser	Cys	Phe	Gln	Gln	Ala	Leu	Ala	Val	Lys		
			340					345					350				
gga	gta	caa	aag	gaa	atg	ggc	aac	taa									1083
Gly	Val	Gln	Lys	Glu	Met	Gly	Asn										
		355				360											

<210> 14  
 <211> 360  
 <212> PRT  
 <213> Glycine max

<400> 14  
 Met Val Thr Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro  
 1 5 10 15

Thr	Glu	Ala	Met	Arg	Ala	Ala	Met	Ala	Ser	Ala	Glu	Val	Asp	Asp	Asp	20	25	30	
Val	Leu	Gly	Tyr	Asp	Pro	Thr	Ala	Phe	Arg	Leu	Glu	Thr	Glu	Met	Ala	35	40	45	
Lys	Thr	Met	Gly	Lys	Glu	Ala	Ala	Leu	Phe	Val	Pro	Ser	Gly	Thr	Met	50	55	60	
Gly	Asn	Leu	Val	Ser	Val	Leu	Val	His	Cys	Asp	Val	Arg	Gly	Ser	Glu	65	70	75	80
Val	Ile	Leu	Gly	Asp	Asn	Cys	His	Ile	Asn	Ile	Phe	Glu	Asn	Gly	Gly	85	90	95	
Ile	Ala	Thr	Ile	Gly	Gly	Val	His	Pro	Arg	Gln	Val	Lys	Asn	Asn	Asp	100	105	110	
Asp	Gly	Thr	Met	Asp	Ile	Asp	Leu	Ile	Glu	Ala	Ala	Ile	Arg	Asp	Pro	115	120	125	
Met	Gly	Glu	Leu	Phe	Tyr	Pro	Thr	Thr	Lys	Leu	Ile	Cys	Leu	Glu	Asn	130	135	140	
Thr	His	Ala	Asn	Ser	Gly	Gly	Arg	Cys	Leu	Ser	Val	Glu	Tyr	Thr	Asp	145	150	155	160
Arg	Val	Gly	Glu	Leu	Ala	Lys	Lys	His	Gly	Leu	Lys	Leu	His	Ile	Asp	165	170	175	
Gly	Ala	Arg	Ile	Phe	Asn	Ala	Ser	Val	Ala	Leu	Gly	Val	Pro	Val	Asp	180	185	190	
Arg	Leu	Val	Gln	Ala	Ala	Asp	Ser	Val	Ser	Val	Cys	Leu	Ser	Lys	Gly	195	200	205	
Ile	Gly	Ala	Pro	Val	Gly	Ser	Val	Ile	Val	Gly	Ser	Lys	Asn	Phe	Ile	210	215	220	
Ala	Lys	Ala	Arg	Arg	Leu	Arg	Lys	Thr	Leu	Gly	Gly	Gly	Met	Arg	Gln	225	230	235	240
Ile	Gly	Leu	Leu	Cys	Ala	Ala	Ala	Leu	Val	Ala	Leu	Gln	Glu	Asn	Val	245	250	255	
Gly	Lys	Leu	Glu	Ser	Asp	His	Lys	Lys	Ala	Arg	Leu	Leu	Ala	Asp	Gly	260	265	270	
Leu	Asn	Glu	Val	Lys	Gly	Leu	Arg	Val	Asp	Ala	Cys	Ser	Val	Glu	Thr	275	280	285	
Asn	Met	Val	Phe	Ile	Asp	Ile	Glu	Glu	Gly	Thr	Lys	Thr	Arg	Ala	Glu	290	295	300	
Lys	Ile	Cys	Lys	Tyr	Met	Glu	Glu	Arg	Gly	Ile	Leu	Val	Met	Gln	Glu	305	310	315	320



Ser Ser Ser Arg Met Arg Val Val Leu His His Gln Ile Ser Ala Ser  
                   325                  330                  335

Asp Val Gln Tyr Ala Leu Ser Cys Phe Gln Gln Ala Leu Ala Val Lys  
                   340                  345                  350

Gly Val Gln Lys Glu Met Gly Asn  
                   355                  360

<210> 15  
 <211> 1077  
 <212> DNA  
 <213> Brassica napus

<220>  
 <221> CDS  
 <222> (1)..(1077)  
 <223> Threonine aldolase

<400> 15  
 atg gtg atg cga act gtg gat cta cgg tca gac acc gtg act aga cct 48  
 Met Val Met Arg Thr Val Asp Leu Arg Ser Asp Thr Val Thr Arg Pro  
 1                  5                  10                  15

acc gat gcc atg cgt gaa gca atg gga agc gca gaa gta gac gat gac 96  
 Thr Asp Ala Met Arg Glu Ala Met Gly Ser Ala Glu Val Asp Asp Asp  
                   20                  25                  30

gtc ctc ggc tac gac cca acg gct cga cgt ctt gaa gag gag ata gcc 144  
 Val Leu Gly Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Glu Ile Ala  
                   35                  40                  45

aag atg atg ggg aaa gaa gca gct ctc ttc gtg cca tct ggt aca atg 192  
 Lys Met Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met  
                   50                  55                  60

ggg aac ctc ata tgc gtt atg gtt cac tgc gac gtg aga ggc agc gag 240  
 Gly Asn Leu Ile Cys Val Met Val His Cys Asp Val Arg Gly Ser Glu  
 65                  70                  75                  80

gtg att ctt gga gac aac tgt cac atc cat gtc tac gag aac gga ggg 288  
 Val Ile Leu Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly  
                   85                  90                  95

ata tca acg ata gga ggc gtg cat ccc aag aca atc aag aat gaa gaa 336  
 Ile Ser Thr Ile Gly Gly Val His Pro Lys Thr Ile Lys Asn Glu Glu  
                   100                  105                  110

gac ggg aca atg gac ttg ggg gct ata gaa gca gct att aga gat cct 384  
 Asp Gly Thr Met Asp Leu Gly Ala Ile Glu Ala Ala Ile Arg Asp Pro  
                   115                  120                  125

aaa gga agc acg ttt tat cca tca aca agg ttg att tgt ttg gag aac 432  
 Lys Gly Ser Thr Phe Tyr Pro Ser Thr Arg Leu Ile Cys Leu Glu Asn  
                   130                  135                  140

aca cat gcc aac tct ggt ggg aga tgt ttg agt gcg gaa tac aca gat Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Ala Glu Tyr Thr Asp 145 150 155 160	480
aga gtt gga gag att gcc aag aga cat gga tta aag ctt cat atc gat Arg Val Gly Glu Ile Ala Lys Arg His Gly Leu Lys Leu His Ile Asp 165 170 175	528
gga gct cgc ctt ttt aat gct tcc att gca ctt gga gtt cca gtc cat Gly Ala Arg Leu Phe Asn Ala Ser Ile Ala Leu Gly Val Pro Val His 180 185 190	576
agg ctt gta cag gct gct gac tct gtt tcg gtg tgt ctc tct aaa ggt Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys Leu Ser Lys Gly 195 200 205	624
ctt gga gct cca ata gga tct gta gtc gtt ggt tca cag agt ttc ata Leu Gly Ala Pro Ile Gly Ser Val Val Val Gly Ser Gln Ser Phe Ile 210 215 220	672
gaa aag gcg aaa acg tta aga aaa aca tta ggt gga gga atg aga caa Glu Lys Ala Lys Thr Leu Arg Lys Thr Leu Gly Gly Gly Met Arg Gln 225 230 235 240	720
ata ggc gtc ctg tgc gca gcc gct ttg gtc gca ctt caa gag aat ctc Ile Gly Val Leu Cys Ala Ala Ala Leu Val Ala Leu Gln Glu Asn Leu 245 250 255	768
cca aag tta caa ttt gac cac aag aag aca aaa ttg tta gct gaa ggg Pro Lys Leu Gln Phe Asp His Lys Lys Thr Lys Leu Leu Ala Glu Gly 260 265 270	816
ttg aat caa atg aaa ggg att aga gtg aac gtt gca gcc atg gag acc Leu Asn Gln Met Lys Gly Ile Arg Val Asn Val Ala Ala Met Glu Thr 275 280 285	864
aac atg ata ttc atg gat atg gag gat gga tca aaa ctg acc gct gaa Asn Met Ile Phe Met Asp Met Glu Asp Gly Ser Lys Leu Thr Ala Glu 290 295 300	912
aaa ctc cgc aag agt cta acg gag cat ggc att ctc gtc atc cct gaa Lys Leu Arg Lys Ser Leu Thr Glu His Gly Ile Leu Val Ile Pro Glu 305 310 315 320	960
aac tct acc cga atc aga atg gtt cta cac cac cag ata aca aca agt Asn Ser Thr Arg Ile Arg Met Val Leu His His Gln Ile Thr Thr Ser 325 330 335	1008
gat gtg cat tac aca ttg tct tgc tta caa caa gca gtg cag acg att Asp Val His Tyr Thr Leu Ser Cys Leu Gln Gln Ala Val Gln Thr Ile 340 345 350	1056
cat gaa cca tgc caa aac taa His Glu Pro Cys Gln Asn 355	1077

<210> 16  
 <211> 358  
 <212> PRT  
 <213> Brassica napus

<400> 16  
 Met Val Met Arg Thr Val Asp Leu Arg Ser Asp Thr Val Thr Arg Pro  
 1 5 10 15  
 Thr Asp Ala Met Arg Glu Ala Met Gly Ser Ala Glu Val Asp Asp Asp  
 20 25 30  
 Val Leu Gly Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Glu Ile Ala  
 35 40 45  
 Lys Met Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met  
 50 55 60  
 Gly Asn Leu Ile Cys Val Met Val His Cys Asp Val Arg Gly Ser Glu  
 65 70 75 80  
 Val Ile Leu Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly  
 85 90 95  
 Ile Ser Thr Ile Gly Gly Val His Pro Lys Thr Ile Lys Asn Glu Glu  
 100 105 110  
 Asp Gly Thr Met Asp Leu Gly Ala Ile Glu Ala Ala Ile Arg Asp Pro  
 115 120 125  
 Lys Gly Ser Thr Phe Tyr Pro Ser Thr Arg Leu Ile Cys Leu Glu Asn  
 130 135 140  
 Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Ala Glu Tyr Thr Asp  
 145 150 155 160  
 Arg Val Gly Glu Ile Ala Lys Arg His Gly Leu Lys Leu His Ile Asp  
 165 170 175  
 Gly Ala Arg Leu Phe Asn Ala Ser Ile Ala Leu Gly Val Pro Val His  
 180 185 190  
 Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys Leu Ser Lys Gly  
 195 200 205  
 Leu Gly Ala Pro Ile Gly Ser Val Val Val Gly Ser Gln Ser Phe Ile  
 210 215 220  
 Glu Lys Ala Lys Thr Leu Arg Lys Thr Leu Gly Gly Gly Met Arg Gln  
 225 230 235 240  
 Ile Gly Val Leu Cys Ala Ala Ala Leu Val Ala Leu Gln Glu Asn Leu  
 245 250 255  
 Pro Lys Leu Gln Phe Asp His Lys Lys Thr Lys Leu Leu Ala Glu Gly  
 260 265 270

Leu Asn Gln Met Lys Gly Ile Arg Val Asn Val Ala Ala Met Glu Thr  
 275 280 285  
 Asn Met Ile Phe Met Asp Met Glu Asp Gly Ser Lys Leu Thr Ala Glu  
 290 295 300  
 Lys Leu Arg Lys Ser Leu Thr Glu His Gly Ile Leu Val Ile Pro Glu  
 305 310 315 320  
 Asn Ser Thr Arg Ile Arg Met Val Leu His His Gln Ile Thr Thr Ser  
 325 330 335  
 Asp Val His Tyr Thr Leu Ser Cys Leu Gln Gln Ala Val Gln Thr Ile  
 340 345 350  
 His Glu Pro Cys Gln Asn  
 355

<210> 17  
 <211> 570  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> CDS  
 <222> (1)..(570)  
 <223> Lysine decarboxylase

<400> 17  
 atg gaa ata agg gtt tca aag ttc aag agg att tgt gtc ttc tgt ggg 48  
 Met Glu Ile Arg Val Ser Lys Phe Lys Arg Ile Cys Val Phe Cys Gly  
 1 5 10 15  
 agt agc cct ggc aaa aag aga agc tac caa gat gct gcc att gaa ctt 96  
 Ser Ser Pro Gly Lys Lys Arg Ser Tyr Gln Asp Ala Ala Ile Glu Leu  
 20 25 30  
 ggc aat gaa ttg gtc tca agg aac att gat ctg gtg tat gga ggg gga 144  
 Gly Asn Glu Leu Val Ser Arg Asn Ile Asp Leu Val Tyr Gly Gly Gly  
 35 40 45  
 agc att ggt cta atg ggt tta gtt tca caa gct gtt cat gat ggc ggt 192  
 Ser Ile Gly Leu Met Gly Leu Val Ser Gln Ala Val His Asp Gly Gly  
 50 55 60  
 cgg cat gtc atc gga gtt att ccc aag acc ctc atg cct cga gag cta 240  
 Arg His Val Ile Gly Val Ile Pro Lys Thr Leu Met Pro Arg Glu Leu  
 65 70 75 80  
 act ggt gaa aca gtg gga gaa gta aaa gct gtt gct gat atg cac caa 288  
 Thr Gly Glu Thr Val Gly Glu Val Lys Ala Val Ala Asp Met His Gln  
 85 90 95  
 agg aag gca gag atg gcc aag cat tca gac gcc ttt att gcc tta cca 336  
 Arg Lys Ala Glu Met Ala Lys His Ser Asp Ala Phe Ile Ala Leu Pro

100	105	110	
ggt gga tat ggg act cta gag gag ctt ctt gaa gtc ata acc tgg gca			384
Gly Gly Tyr Gly Thr Leu Glu Glu Leu Leu Glu Val Ile Thr Trp Ala			
115	120	125	
caa ctt ggg att cat gac aag ccg gtg gga tta gta aat gtt gat gga			432
Gln Leu Gly Ile His Asp Lys Pro Val Gly Leu Val Asn Val Asp Gly			
130	135	140	
tac ttt aat tcc ttg ctg tca ttt att gac aaa gct gtg gaa gag gga			480
Tyr Phe Asn Ser Leu Leu Ser Phe Ile Asp Lys Ala Val Glu Glu Gly			
145	150	155	160
ttt atc agt cca aat gct cgc cac ata att gta tca gca ccc aca gca			528
Phe Ile Ser Pro Asn Ala Arg His Ile Ile Val Ser Ala Pro Thr Ala			
165	170	175	
aaa gag ttg gtg aag aaa ttg gag gat tac gtt ccc tgt taa			570
Lys Glu Leu Val Lys Lys Leu Glu Asp Tyr Val Pro Cys			
180	185		
<210> 18			
<211> 189			
<212> PRT			
<213> Glycine max			
<400> 18			
Met Glu Ile Arg Val Ser Lys Phe Lys Arg Ile Cys Val Phe Cys Gly			
1	5	10	15
Ser Ser Pro Gly Lys Lys Arg Ser Tyr Gln Asp Ala Ala Ile Glu Leu			
20	25	30	
Gly Asn Glu Leu Val Ser Arg Asn Ile Asp Leu Val Tyr Gly Gly Gly			
35	40	45	
Ser Ile Gly Leu Met Gly Leu Val Ser Gln Ala Val His Asp Gly Gly			
50	55	60	
Arg His Val Ile Gly Val Ile Pro Lys Thr Leu Met Pro Arg Glu Leu			
65	70	75	80
Thr Gly Glu Thr Val Gly Glu Val Lys Ala Val Ala Asp Met His Gln			
85	90	95	
Arg Lys Ala Glu Met Ala Lys His Ser Asp Ala Phe Ile Ala Leu Pro			
100	105	110	
Gly Gly Tyr Gly Thr Leu Glu Glu Leu Leu Glu Val Ile Thr Trp Ala			
115	120	125	
Gln Leu Gly Ile His Asp Lys Pro Val Gly Leu Val Asn Val Asp Gly			
130	135	140	
Tyr Phe Asn Ser Leu Leu Ser Phe Ile Asp Lys Ala Val Glu Glu Gly			

145		150		155		160
Phe Ile Ser Pro Asn Ala Arg His Ile Ile Val Ser Ala Pro Thr Ala						
		165		170		175
Lys Glu Leu Val Lys Lys Leu Glu Asp Tyr Val Pro Cys						
		180		185		

<210> 19  
 <211> 675  
 <212> DNA  
 <213> Hordeum vulgare

<220>  
 <221> CDS  
 <222> (1)..(675)  
 <223> Lysine decarboxylase

<400> 19	
atg ggc gac acc acc gcg ccc tcg ccg ccg agg agg ttc ggc agg atc	48
Met Gly Asp Thr Thr Ala Pro Ser Pro Pro Arg Arg Phe Gly Arg Ile	
1 5 10 15	
tgc gtc ttc tgc ggc agg aac tcc ggc aac cgc gcc gtg ttc ggc gac	96
Cys Val Phe Cys Gly Arg Asn Ser Gly Asn Arg Ala Val Phe Gly Asp	
20 25 30	
gcc gcg ctc gag ctc ggc cag ggc ctg gtg acg agg ggg gtc gat ctg	144
Ala Ala Leu Glu Leu Gly Gln Gly Leu Val Thr Arg Gly Val Asp Leu	
35 40 45	
gtc tac ggc ggc ggc agt atc ggg ctg atg ggc ctg atc gcg cag acg	192
Val Tyr Gly Gly Gly Ser Ile Gly Leu Met Gly Leu Ile Ala Gln Thr	
50 55 60	
gtt ctc gac ggc ggc tgc cgc gtc ctc ggg gtg att cca aga gca ctc	240
Val Leu Asp Gly Gly Cys Arg Val Leu Gly Val Ile Pro Arg Ala Leu	
65 70 75 80	
atg ccc ctc gag ata tcc ggt gca agt gtt gga gaa gta aag att gtc	288
Met Pro Leu Glu Ile Ser Gly Ala Ser Val Gly Glu Val Lys Ile Val	
85 90 95	
tcc gac atg cat gag agg aaa gct gag atg gcg cga caa gcc gat gca	336
Ser Asp Met His Glu Arg Lys Ala Glu Met Ala Arg Gln Ala Asp Ala	
100 105 110	
ttc att gct ctt ccg ggt ggg tat gga aca atg gaa gag ctg gta gag	384
Phe Ile Ala Leu Pro Gly Gly Tyr Gly Thr Met Glu Glu Leu Val Glu	
115 120 125	
atg atc act tgg tcg cag ctt gga atc cat gac aaa ccg gtc ggg ttg	432
Met Ile Thr Trp Ser Gln Leu Gly Ile His Asp Lys Pro Val Gly Leu	
130 135 140	

cta aac gtc gat ggg tac tat gat ccg tta ctc gcg ctg ttc gac aag 480  
 Leu Asn Val Asp Gly Tyr Tyr Asp Pro Leu Leu Ala Leu Phe Asp Lys  
 145 150 155 160

ggc gcg ggg gaa ggg ttt ttt aag gcc gat tgc agg ccg ata atc gtg 528  
 Gly Ala Gly Glu Gly Phe Phe Lys Ala Asp Cys Arg Pro Ile Ile Val  
 165 170 175

tcg gca cca act gcc cac gaa ctg ctg aca aaa atg gag caa tac acc 576  
 Ser Ala Pro Thr Ala His Glu Leu Leu Thr Lys Met Glu Gln Tyr Thr  
 180 185 190

cgt tca ccc cgg gag gtg gcc tcg cgg acg agc tgg gag atg acc gag 624  
 Arg Ser Pro Arg Glu Val Ala Ser Arg Thr Ser Trp Glu Met Thr Glu  
 195 200 205

atg ggc tcc ggg aaa gca ccg gag ccg gag gag gag gcg gcg gca tcg 672  
 Met Gly Ser Gly Lys Ala Pro Glu Pro Glu Glu Glu Ala Ala Ala Ser  
 210 215 220

taa 675

<210> 20  
 <211> 224  
 <212> PRT  
 <213> Hordeum vulgare

<400> 20  
 Met Gly Asp Thr Thr Ala Pro Ser Pro Pro Arg Arg Phe Gly Arg Ile  
 1 5 10 15

Cys Val Phe Cys Gly Arg Asn Ser Gly Asn Arg Ala Val Phe Gly Asp  
 20 25 30

Ala Ala Leu Glu Leu Gly Gln Gly Leu Val Thr Arg Gly Val Asp Leu  
 35 40 45

Val Tyr Gly Gly Gly Ser Ile Gly Leu Met Gly Leu Ile Ala Gln Thr  
 50 55 60

Val Leu Asp Gly Gly Cys Arg Val Leu Gly Val Ile Pro Arg Ala Leu  
 65 70 75 80

Met Pro Leu Glu Ile Ser Gly Ala Ser Val Gly Glu Val Lys Ile Val  
 85 90 95

Ser Asp Met His Glu Arg Lys Ala Glu Met Ala Arg Gln Ala Asp Ala  
 100 105 110

Phe Ile Ala Leu Pro Gly Gly Tyr Gly Thr Met Glu Glu Leu Val Glu  
 115 120 125

Met Ile Thr Trp Ser Gln Leu Gly Ile His Asp Lys Pro Val Gly Leu  
 130 135 140

Leu Asn Val Asp Gly Tyr Tyr Asp Pro Leu Leu Ala Leu Phe Asp Lys  
 145 150 155 160  
 Gly Ala Gly Glu Gly Phe Phe Lys Ala Asp Cys Arg Pro Ile Ile Val  
 165 170 175  
 Ser Ala Pro Thr Ala His Glu Leu Leu Thr Lys Met Glu Gln Tyr Thr  
 180 185 190  
 Arg Ser Pro Arg Glu Val Ala Ser Arg Thr Ser Trp Glu Met Thr Glu  
 195 200 205  
 Met Gly Ser Gly Lys Ala Pro Glu Pro Glu Glu Glu Ala Ala Ala Ser  
 210 215 220

<210> 21  
 <211> 717  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(717)  
 <223> Lysine decarboxylase

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 Met Glu Glu Asn Gln Glu Lys Phe Ala Pro Glu Ser Ser Gly Gly Asp  
 1 5 10 15  
  
 ggt ggt ggc tcg gtg aga acg atc tgc gtc ttc tgc ggc agc agg ccg 96  
 Gly Gly Gly Ser Val Arg Thr Ile Cys Val Phe Cys Gly Ser Arg Pro  
 20 25 30  
  
 ggg aac cgg ccg tcc ttc agc gct gcg gcg ctc gac ctg ggg aag cag 144  
 Gly Asn Arg Pro Ser Phe Ser Ala Ala Ala Leu Asp Leu Gly Lys Gln  
 35 40 45  
  
 ctg gtc gag agg cag atg aac ctg gtg tac ggc ggc ggc agc ggc ggc 192  
 Leu Val Glu Arg Gln Met Asn Leu Val Tyr Gly Gly Gly Ser Gly Gly  
 50 55 60  
  
 ctg atg ggc ctg gtg tcc aag gcc gtc tac gaa ggc ggc cgc cac gtc 240  
 Leu Met Gly Leu Val Ser Lys Ala Val Tyr Glu Gly Gly Arg His Val  
 65 70 75 80  
  
 ctc ggg gtc atc cct acc gcc ctc cta cct gaa gag gtg tca ggg gag 288  
 Leu Gly Val Ile Pro Thr Ala Leu Leu Pro Glu Glu Val Ser Gly Glu  
 85 90 95  
  
 aca ttg gga gag gtg aaa gtg gtc agg gac atg cat cag cgc aag gcg 336  
 Thr Leu Gly Glu Val Lys Val Val Arg Asp Met His Gln Arg Lys Ala  
 100 105 110  
  
 gaa atg gcg aaa cat gcc gac gct ttc atc gcc ctg cca ggt ggt tac 384



Glu Met Ala Lys His Ala Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr	
115 120 125	
ggg aca atc gaa gaa ctg ctg gag atc ata gcg tgg gcg cag ctg ggc	432
Gly Thr Ile Glu Glu Leu Leu Glu Ile Ile Ala Trp Ala Gln Leu Gly	
130 135 140	
atc cac agc aaa ccg gtg ggg ttg ctc aac gtg gac ggc tac tac aac	480
Ile His Ser Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asn	
145 150 155 160	
agc ctg ctc tcg ctg ttc gac aag gct gtc gag gag ggc ttc atc gac	528
Ser Leu Leu Ser Leu Phe Asp Lys Ala Val Glu Glu Gly Phe Ile Asp	
165 170 175	
acc aag gca cgg aac atc ttc gtc ctc gct gac acc gcc gcc gac ctg	576
Thr Lys Ala Arg Asn Ile Phe Val Leu Ala Asp Thr Ala Ala Asp Leu	
180 185 190	
ctg act agg ctc acc atg atg gcg cgc ctg gca gcc gac gac gac gat	624
Leu Thr Arg Leu Thr Met Met Ala Arg Leu Ala Ala Asp Asp Asp Asp	
195 200 205	
gct act act acc ccc aga gga gac gga gac gga gac gga gac gaa cac	672
Ala Thr Thr Thr Pro Arg Gly Asp Gly Asp Gly Asp Gly Asp Glu His	
210 215 220	
aag ggg gcc acc acc gct gca ggc gtc aaa agg aaa agg ggc taa	717
Lys Gly Ala Thr Thr Ala Ala Gly Val Lys Arg Lys Arg Gly	
225 230 235	

<210> 22  
 <211> 238  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Artificial

<400> 22	
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20 25 30	
Gly Asn Arg Pro Ser Phe Ser Ala Ala Ala Leu Asp Leu Gly Lys Gln	
35 40 45	
Leu Val Glu Arg Gln Met Asn Leu Val Tyr Gly Gly Gly Ser Gly Gly	
50 55 60	
Leu Met Gly Leu Val Ser Lys Ala Val Tyr Glu Gly Gly Arg His Val	
65 70 75 80	
Leu Gly Val Ile Pro Thr Ala Leu Leu Pro Glu Glu Val Ser Gly Glu	

				85				90				95				
Thr	Leu	Gly	Glu	Val	Lys	Val	Val	Arg	Asp	Met	His	Gln	Arg	Lys	Ala	
			100					105					110			
Glu	Met	Ala	Lys	His	Ala	Asp	Ala	Phe	Ile	Ala	Leu	Pro	Gly	Gly	Tyr	
			115					120					125			
Gly	Thr	Ile	Glu	Glu	Leu	Leu	Glu	Ile	Ile	Ala	Trp	Ala	Gln	Leu	Gly	
			130					135					140			
Ile	His	Ser	Lys	Pro	Val	Gly	Leu	Leu	Asn	Val	Asp	Gly	Tyr	Tyr	Asn	
145					150					155					160	
Ser	Leu	Leu	Ser	Leu	Phe	Asp	Lys	Ala	Val	Glu	Glu	Gly	Phe	Ile	Asp	
				165					170					175		
Thr	Lys	Ala	Arg	Asn	Ile	Phe	Val	Leu	Ala	Asp	Thr	Ala	Ala	Asp	Leu	
			180					185					190			
Leu	Thr	Arg	Leu	Thr	Met	Met	Ala	Arg	Leu	Ala	Ala	Asp	Asp	Asp	Asp	
			195					200					205			
Ala	Thr	Thr	Thr	Pro	Arg	Gly	Asp	Gly	Asp	Gly	Asp	Gly	Asp	Glu	His	
			210					215					220			
Lys	Gly	Ala	Thr	Thr	Ala	Ala	Gly	Val	Lys	Arg	Lys	Arg	Gly			
225					230					235						

<210>	23
<211>	717
<212>	DNA
<213>	Zea mays

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<220>
<221> CDS
<222> (1)..(717)
<223> Lysine decarboxylase
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Met	Glu	Glu	Asn	Gln	Glu	Lys	Phe	Ala	Pro	Glu	Ser	Ser	Gly	Gly	Asp		
1				5					10					15			
ggt	ggt	ggc	tcg	gtg	aga	acg	atc	tgc	gtc	ttc	tgc	ggc	agc	agg	ccg	96	
Gly	Gly	Gly	Ser	Val	Arg	Thr	Ile	Cys	Val	Phe	Cys	Gly	Ser	Arg	Pro		
			20					25					30				
ggg	aac	cgg	ccg	tcc	ttc	agc	gct	gcg	gcg	ctc	gac	ctg	ggg	aag	cag	144	
Gly	Asn	Arg	Pro	Ser	Phe	Ser	Ala	Ala	Ala	Leu	Asp	Leu	Gly	Lys	Gln		
		35					40					45					
ctg	gtc	gag	agg	cag	atg	aac	ctg	gtg	tac	ggc	ggc	ggc	agc	ggc	ggg	192	
Leu	Val	Glu	Arg	Gln	Met	Asn	Leu	Val	Tyr	Gly	Gly	Gly	Ser	Gly	Gly		
	50					55					60						

ctg atg ggc ctg gtg tcc aag gcc gtc tac gaa ggc ggc cgc cac gtc 240  
 Leu Met Gly Leu Val Ser Lys Ala Val Tyr Glu Gly Gly Arg His Val  
 65 70 75 80

ctc ggg gtc atc cct acc gcc ctc cta cct gaa gag gtg tca ggg gag 288  
 Leu Gly Val Ile Pro Thr Ala Leu Leu Pro Glu Glu Val Ser Gly Glu  
 85 90 95

aca ttg gga gag gtg aaa gtg gtc agg gac atg cat cag cgc aag gcg 336  
 Thr Leu Gly Glu Val Lys Val Val Arg Asp Met His Gln Arg Lys Ala  
 100 105 110

gaa atg gcg aaa cat gcc gac gct ttc atc gcc ctg cca ggt ggt tac 384  
 Glu Met Ala Lys His Ala Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr  
 115 120 125

ggg aca atc gaa gaa ctg ctg gag atc ata gcg tgg gcg cag ctg ggc 432  
 Gly Thr Ile Glu Glu Leu Leu Glu Ile Ile Ala Trp Ala Gln Leu Gly  
 130 135 140

atc cac agc aaa ccg gtg ggg ttg ctc aac gtg gac ggc tac tac aac 480  
 Ile His Ser Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asn  
 145 150 155 160

agc ctg ctc tcg ctg ttc gac aag gct gtc gag gag ggc ttc atc gac 528  
 Ser Leu Leu Ser Leu Phe Asp Lys Ala Val Glu Glu Gly Phe Ile Asp  
 165 170 175

acc aag gca cgg aac atc ttc gtc ctc gct gac acc gcc gcc gac ctg 576  
 Thr Lys Ala Arg Asn Ile Phe Val Leu Ala Asp Thr Ala Ala Asp Leu  
 180 185 190

ctg act agg ctc acc atg atg gcg cgc ctg gca gcc gac gac gac gat 624  
 Leu Thr Arg Leu Thr Met Met Ala Arg Leu Ala Ala Asp Asp Asp  
 195 200 205

gct act act acc ccc aga gga gac gga gac gga gac gga gac gaa cac 672  
 Ala Thr Thr Thr Pro Arg Gly Asp Gly Asp Gly Asp Gly Asp Glu His  
 210 215 220

aag ggg gcc acc acc gct gca ggc gtc aaa agg aaa agg ggc taa 717  
 Lys Gly Ala Thr Thr Ala Ala Gly Val Lys Arg Lys Arg Gly  
 225 230 235

<210> 24  
 <211> 238  
 <212> PRT  
 <213> Zea mays

<400> 24  
 Met Glu Glu Asn Gln Glu Lys Phe Ala Pro Glu Ser Ser Gly Gly Asp  
 1 5 10 15  
 Gly Gly Gly Ser Val Arg Thr Ile Cys Val Phe Cys Gly Ser Arg Pro  
 20 25 30

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		35					40					45			
Leu	Val	Glu	Arg	Gln	Met	Asn	Leu	Val	Tyr	Gly	Gly	Gly	Ser	Gly	Gly
	50					55					60				
Leu	Met	Gly	Leu	Val	Ser	Lys	Ala	Val	Tyr	Glu	Gly	Gly	Arg	His	Val
65					70					75					80
Leu	Gly	Val	Ile	Pro	Thr	Ala	Leu	Leu	Pro	Glu	Glu	Val	Ser	Gly	Glu
				85					90					95	
Thr	Leu	Gly	Glu	Val	Lys	Val	Val	Arg	Asp	Met	His	Gln	Arg	Lys	Ala
			100					105					110		
Glu	Met	Ala	Lys	His	Ala	Asp	Ala	Phe	Ile	Ala	Leu	Pro	Gly	Gly	Tyr
		115					120					125			
Gly	Thr	Ile	Glu	Glu	Leu	Leu	Glu	Ile	Ile	Ala	Trp	Ala	Gln	Leu	Gly
	130					135					140				
Ile	His	Ser	Lys	Pro	Val	Gly	Leu	Leu	Asn	Val	Asp	Gly	Tyr	Tyr	Asn
145					150					155					160
Ser	Leu	Leu	Ser	Leu	Phe	Asp	Lys	Ala	Val	Glu	Glu	Gly	Phe	Ile	Asp
				165					170					175	
Thr	Lys	Ala	Arg	Asn	Ile	Phe	Val	Leu	Ala	Asp	Thr	Ala	Ala	Asp	Leu
			180					185					190		
Leu	Thr	Arg	Leu	Thr	Met	Met	Ala	Arg	Leu	Ala	Ala	Asp	Asp	Asp	Asp
		195					200					205			
Ala	Thr	Thr	Thr	Pro	Arg	Gly	Asp	Gly	Asp	Gly	Asp	Gly	Asp	Glu	His
	210					215						220			
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225					230					235					

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<210> 25
<211> 672
<212> DNA
<213> Oryza sativa
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<220>
<221> CDS
<222> (1)..(672)
<223> Lysine decarboxylase
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1 5 10 15

agg ttc ggc agg atc tgc gtc ttc tgc ggc agc aac gcc ggc aac cgc 96  
Arg Phe Gly Arg Ile Cys Val Phe Cys Gly Ser Asn Ala Gly Asn Arg

20	25	30	
gcg gtg ttc ggc gac gcg gcg ctc cag ctc ggg cag gag ctg gtg tcg Ala Val Phe Gly Asp Ala Ala Leu Gln Leu Gly Gln Glu Leu Val Ser 35 40 45			144
aga ggg atc gag ttg gtc tac ggt ggc ggc agc gtc ggg ttg atg ggc Arg Gly Ile Glu Leu Val Tyr Gly Gly Gly Ser Val Gly Leu Met Gly 50 55 60			192
ttg atc gcg cag acg gtt ctt gat ggc ggc tgc ggt gtt ctc ggg gtg Leu Ile Ala Gln Thr Val Leu Asp Gly Gly Cys Gly Val Leu Gly Val 65 70 75 80			240
att cca aaa gca ctt atg ccc acc gag ata tca ggt gca agt gtt gga Ile Pro Lys Ala Leu Met Pro Thr Glu Ile Ser Gly Ala Ser Val Gly 85 90 95			288
gaa gtg aaa att gtg tct gac atg cat gag agg aaa gct gag atg gca Glu Val Lys Ile Val Ser Asp Met His Glu Arg Lys Ala Glu Met Ala 100 105 110			336
cgc caa tcc gat gcc ttc atc gct ctt cct gga ggg tat gga aca atg Arg Gln Ser Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr Gly Thr Met 115 120 125			384
gag gag ttg tta gag atg ata act tgg tca caa ctt gga att cat gac Glu Glu Leu Leu Glu Met Ile Thr Trp Ser Gln Leu Gly Ile His Asp 130 135 140			432
aaa cca gtt ggg ttg ctg aat gtg gac ggt tac tat gat ccg ttg ctt Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asp Pro Leu Leu 145 150 155 160			480
gcg cta ttt gat aag ggt gcg gca gaa gga ttt att aag gcc gat tgc Ala Leu Phe Asp Lys Gly Ala Ala Glu Gly Phe Ile Lys Ala Asp Cys 165 170 175			528
aga caa ata att gtt tcg gca ccg act gcg cat gag ctg ctg aga aag Arg Gln Ile Ile Val Ser Ala Pro Thr Ala His Glu Leu Leu Arg Lys 180 185 190			576
atg gag caa tac act cgt tca cac cag gag gta gcg cca cgt aca agc Met Glu Gln Tyr Thr Arg Ser His Gln Glu Val Ala Pro Arg Thr Ser 195 200 205			624
tgg gag atg tca gag ctt ggt tat gga aag aca cca gag gaa tcg taa Trp Glu Met Ser Glu Leu Gly Tyr Gly Lys Thr Pro Glu Glu Ser 210 215 220			672

<210> 26  
 <211> 223  
 <212> PRT  
 <213> Oryza sativa

&lt;400&gt; 26

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Arg	Phe	Gly	Arg	Ile	Cys	Val	Phe	Cys	Gly	Ser	Asn	Ala	Gly	Asn	Arg	20	25	30	
Ala	Val	Phe	Gly	Asp	Ala	Ala	Leu	Gln	Leu	Gly	Gln	Glu	Leu	Val	Ser	35	40	45	
Arg	Gly	Ile	Glu	Leu	Val	Tyr	Gly	Gly	Gly	Ser	Val	Gly	Leu	Met	Gly	50	55	60	
Leu	Ile	Ala	Gln	Thr	Val	Leu	Asp	Gly	Gly	Cys	Gly	Val	Leu	Gly	Val	65	70	75	80
Ile	Pro	Lys	Ala	Leu	Met	Pro	Thr	Glu	Ile	Ser	Gly	Ala	Ser	Val	Gly	85	90	95	
Glu	Val	Lys	Ile	Val	Ser	Asp	Met	His	Glu	Arg	Lys	Ala	Glu	Met	Ala	100	105	110	
Arg	Gln	Ser	Asp	Ala	Phe	Ile	Ala	Leu	Pro	Gly	Gly	Tyr	Gly	Thr	Met	115	120	125	
Glu	Glu	Leu	Leu	Glu	Met	Ile	Thr	Trp	Ser	Gln	Leu	Gly	Ile	His	Asp	130	135	140	
Lys	Pro	Val	Gly	Leu	Leu	Asn	Val	Asp	Gly	Tyr	Tyr	Asp	Pro	Leu	Leu	145	150	155	160
Ala	Leu	Phe	Asp	Lys	Gly	Ala	Ala	Glu	Gly	Phe	Ile	Lys	Ala	Asp	Cys	165	170	175	
Arg	Gln	Ile	Ile	Val	Ser	Ala	Pro	Thr	Ala	His	Glu	Leu	Leu	Arg	Lys	180	185	190	
Met	Glu	Gln	Tyr	Thr	Arg	Ser	His	Gln	Glu	Val	Ala	Pro	Arg	Thr	Ser	195	200	205	
Trp	Glu	Met	Ser	Glu	Leu	Gly	Tyr	Gly	Lys	Thr	Pro	Glu	Glu	Ser	210	215	220		